FP188. The microbiome of xylem sap associated with almond leaf scorch disease caused by *Xylella fastidiosa* in South-East Spain

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Xylella fastidiosa (XF) is one of the most harmful emerging plant pathogenic bacteria and represents an important threat to agriculture, forestry and landscape worldwide. In June of 2017 XF was reported in almond trees in the province of Alicante, Spain. Metagenomics is a valuable methodology to study the impact of causal agents of plant diseases and their interaction with others naturally occurring microorganism, as part of innovative approaches to mitigate or control the disease. Moreover, endophytic bacteria seem to be a promising biocontrol solution. The objective of the study was to compare healthy and diseased almonds trees infected by XF subsp. multiplex to identify groups of microorganisms that could potentially modulate the almond leaf scorch disease. Almond plots were selected in five municipalities within the demarcated area of XF outbreak. A total of 93 trees were selected and characterized as positive (52) and negative (41) for the presence of XF using official EPPO standard qPCR protocols. The bacterial microbiota was determined from DNA extracted from xylem samples of wood chips based on the V5-V6 region of the bacterial 16S rRNA gene using Illumina's MiSeq sequencing. There was a clear concordance between qPCR results and identification of XF reads in the samples. Within the diseased plants, the relative abundance of XF varied from 0.34% to 92% of total bacterial reads. In total, 152 OTUs were assigned to 11 phyla, 53 families and 86 genera. A core microbiome of 77 OTUs common to healthy (qPCR negative) and diseased (qPCR positive) almond trees was determined were 5 genera accounted for most of the diversity. Disruption in the frequencies of these OTUs occurred on the diseased tree since those predominant genera were less abundant due to the emergence of *Xylella*. Furthermore, 32 and 38 OTUs were unique to healthy or diseased trees, respectively. Our results allow to better understand the interaction between XF and the xylem sap microbiome identifying potential bacteria that could act through direct inhibition or through niche displacement of XF envisioning innovative strategies to control the almond leaf scorch disease.

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